

**Poster 8. Threading the line between GrainGenes and other genome resources.**

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GrainGenes ([graingenes.org](http://graingenes.org)) has long used molecular markers for the comparison of genomes between its related grass species, mainly those of the Triticeae and *Avena*. Available tools have mainly focused on the CMap and GBrowse ([gmod.org](http://gmod.org)) displays. New genome sequence data from other grass species adds to the utility of comparative mapping between the grass species.

With a growing interest in the study of temperate cereals and forage grasses, a new model for the grasses, *Brachypodium distachyon*, has evolved within the research community, some of it leveraged toward bioenergy research. Resources for *Brachypodium* to date include a whole-genome sequence, ESTs, SNPs, a high-density genetic linkage map, and germplasm resources. The high-efficiency transformation system of *Brachypodium* using *Agrobacterium tumefaciens* has yielded a resource of T-DNA insertional mutant lines. Greater than 4,300 T<sub>0</sub> lines have been generated to date, and from these, flanking sequence tag (FSTs) data yielded 1,601 (46.2%) shown to contain *Brachypodium* genomic sequences. As work continues to visually and physically screen these for mutant phenotypes, protocols for working with *Brachypodium*, information about the T-DNA project, and links to seed resources is now available from a website ([brachypodium.pw.usda.gov](http://brachypodium.pw.usda.gov)).

Sequencing the wheat genome is now underway in one form or another. There is a need to develop molecular markers for this complex genome. The complexity of the wheat genome has been leveraged against the abundance of randomly mobilized repetitive sequences, many represented by transposable elements (TE). Software, TEPrimers ([wheat.pw.usda.gov/demos](http://wheat.pw.usda.gov/demos)), was built to recognize this complexity and define candidate repeat junction-junction markers (RJJM) sites, which could predictively be used as unique marker sites. The software has been tested using BAC end sequences and ‘next-generation’ sequences (Roche 454) of wheat. These and other resources that help bind the genomes together will be presented.